Raw Sequence Listing before editing (for reference only)

PCT

RAW SEQUENCE LISTING   DATE: 05/19/2006
PATENT APPLICATION: US/10/521,518   TIME: 08:56:38

        Input Set : A:\294-208 PCT-US sequence listing.txt
        Output Set: N:\CRF4\05192006\J521518.raw

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   3 <110> APPLICANT: Expressive Research B.V.
   5 <120> TITLE OF INVENTION: Modulating developmental pathways in plants
   7 <130> FILE REFERENCE: P59845PC00
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/521,518
C--> 10 <141> CURRENT FILING DATE: 2005-01-18
  12 <150> PRIOR APPLICATION NUMBER: EP 02077908.8
  13 <151> PRIOR FILING DATE: 2002-07-17
  15 <160> NUMBER OF SEQ ID NOS: 110
  17 <170> SOFTWARE: PatentIn version 3.2
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 227
  21 <212> TYPE: PRT
  22 <213> ORGANISM: Arabidopsis thaliana
  24 <400> SEQUENCE: 1
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  27 1               5                   10                  15
  30 Pro Pro Pro Ala Pro Lys Gly Tyr Tyr Arg Arg Gly His Gly Arg Gly
  31             20                  25                  30
  34 Cys Gly Cys Cys Leu Leu Ser Leu Phe Val Lys Val Ile Ile Ser Leu
  35         35                  40                  45
  38 Ile Val Ile Leu Gly Val Ala Ala Leu Ile Phe Trp Leu Ile Val Arg
  39     50                  55                  60
  42 Pro Arg Ala Ile Lys Phe His Val Thr Asp Ala Ser Leu Thr Arg Phe
  43 65                  70                  75                  80
  46 Asp His Thr Ser Pro Asp Asn Ile Leu Arg Tyr Asn Leu Ala Leu Thr
  47             85                  90                  95
  50 Val Pro Val Arg Asn Pro Asn Lys Arg Ile Gly Leu Tyr Tyr Asp Arg
  51             100                 105                 110
  54 Ile Glu Ala His Ala Tyr Tyr Glu Gly Lys Arg Phe Ser Thr Ile Thr
  55         115                 120                 125
  58 Leu Thr Pro Phe Tyr Gln Gly His Lys Asn Thr Thr Val Leu Thr Pro
  59     130                 135                 140
  62 Thr Phe Gln Gly Gln Asn Leu Val Ile Phe Asn Ala Gly Gln Ser Arg
  63 145                 150                 155                 160
  66 Thr Leu Asn Ala Glu Arg Ile Ser Gly Val Tyr Asn Ile Glu Ile Lys
  67             165                 170                 175
  70 Phe Arg Leu Arg Val Arg Phe Lys Leu Gly Asp Leu Lys Phe Arg Arg
  71             180                 185                 190
  74 Ile Lys Pro Lys Val Asp Cys Asp Asp Leu Arg Leu Pro Leu Ser Thr
  75             195                 200                 205
  78 Ser Asn Gly Thr Thr Thr Thr Ser Thr Val Phe Pro Ile Lys Cys Asp
  79     210                 215                 220
  82 Phe Asp Phe
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RAW SEQUENCE LISTING   DATE: 05/19/2006
PATENT APPLICATION: US/10/521,518   TIME: 08:56:38

Input Set : A:\294-208 PCT-US sequence listing.txt
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87 <211> LENGTH: 416
88 <212> TYPE: PRT
89 <213> ORGANISM: Arabidopsis thaliana
91 <400> SEQUENCE: 2
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97 Thr His Phe Asp Leu Glu Ser Asn Asn Asn Leu Gln Tyr Ser Leu Ser
98          20                 25                 30
101 Leu Asn Leu Ser Ile Arg Asn Ser Lys Ser Ser Ile Gly Ile His Tyr
102         35                 40                 45
105 Asp Arg Phe Glu Ala Thr Val Tyr Tyr Met Asn Gln Arg Leu Gly Ala
106     50                 55                 60
109 Val Pro Met Pro Leu Phe Tyr Leu Gly Ser Lys Asn Thr Met Leu Leu
110 65                 70                 75                 80
113 Arg Ala Leu Phe Glu Gly Gln Thr Leu Val Leu Leu Lys Gly Asn Glu
114             85                 90                 95
117 Arg Lys Lys Phe Glu Asp Asp Gln Lys Thr Gly Val Tyr Arg Ile Asp
118         100                105                110
121 Val Lys Leu Ser Ile Asn Phe Arg Val Met Val Leu His Leu Val Thr
122         115                120                125
125 Trp Pro Met Lys Pro Val Val Arg Cys His Leu Lys Ile Pro Leu Ala
126     130                135                140
129 Leu Gly Ser Ser Asn Ser Thr Gly Gly His Lys Lys Met Leu Leu Ile
130 145                150                155                160
133 Gly Gln Leu Val Lys Asp Thr Ser Ala Asn Leu Arg Glu Ala Ser Glu
134             165                170                175
137 Thr Asp His Arg Arg Asp Val Ala Gln Ser Lys Lys Ile Ala Asp Ala
138         180                185                190
141 Lys Leu Ala Lys Asp Phe Glu Ala Ala Leu Lys Glu Phe Gln Lys Ala
142         195                200                205
145 Gln His Ile Thr Val Glu Arg Glu Thr Ser Tyr Ile Pro Phe Asp Pro
146     210                215                220
149 Lys Gly Ser Phe Ser Ser Ser Glu Val Asp Ile Gly Tyr Asp Arg Ser
150 225                230                235                240
153 Gln Glu Gln Arg Val Leu Met Glu Ser Arg Arg Gln Glu Ile Val Leu
154             245                250                255
157 Leu Asp Asn Glu Ile Ser Leu Asn Glu Ala Arg Ile Glu Ala Arg Glu
158             260                265                270
161 Gln Gly Ile Gln Glu Val Lys His Gln Ile Ser Glu Val Met Glu Met
162         275                280                285
165 Phe Lys Asp Leu Ala Val Met Val Asp His Gln Gly Thr Ile Asp Asp
166     290                295                300
169 Ile Asp Glu Lys Ile Asp Asn Leu Arg Ser Ala Ala Ala Gln Gly Lys
170 305                310                315                320
173 Ser His Leu Val Lys Ala Ser Asn Thr Gln Gly Ser Asn Ser Ser Leu
174         325                330                335
177 Leu Phe Ser Cys Ser Leu Leu Leu Phe Phe Phe Leu Ser Gly Asp Leu
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178          340              345              350
181 Cys Arg Cys Val Cys Val Gly Ser Glu Asn Pro Arg Leu Asn Pro Thr
182          355              360              365
185 Arg Arg Lys Ala Trp Cys Glu Glu Glu Asp Glu Glu Gln Arg Lys Lys
186      370              375              380
189 Gln Gln Lys Lys Lys Thr Met Ser Glu Lys Arg Arg Arg Glu Glu Lys
190 385              390              395              400
193 Lys Val Asn Lys Pro Asn Gly Phe Val Phe Cys Val Leu Gly His Lys
194              405              410              415
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198 <211> LENGTH: 1634
199 <212> TYPE: DNA
200 <213> ORGANISM: Arabidopsis thaliana
203 <220> FEATURE:
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205 <222> LOCATION: (501)..(563)
206 <223> OTHER INFORMATION: signal sequence (exon 1)
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (655)..(708)
211 <223> OTHER INFORMATION: propeptide (exon 2)
213 <220> FEATURE:
214 <221> NAME/KEY: CDS
215 <222> LOCATION: (797)..(856)
216 <223> OTHER INFORMATION: propeptide (exon 3)
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (955)..(1131)
221 <223> OTHER INFORMATION: conserved cysteine motif (exon 4)
223 <400> SEQUENCE: 3
224 attaaacgcc aaacactaca tctgtgtttt cgaacaatat tgcgtctgcg tttccttcat      60
226 ctatctctct cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac     120
228 ataaactacc aaagtatcaa gctaatgtaa aaattactct catttccacg taacaaattg     180
230 agttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcatc     240
232 ctccgaaaaa agggaaccaa tcaaaactgt ttgcatatca aactccaaca ctttacagca     300
234 aatgcaatct ataatctgtg atttatccaa taaaaacctg tgatttatgt ttggctccag     360
236 cgatgaaagt ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa     420
238 gtagctgaaa tgtatctata taaagaatca tccacaagta ctattttcac acactacttc     480
240 aaaatcacta ctcaagaaat atg aag aag atg aat gtg gtg gct ttt gtt acg     533
241                         Met Lys Lys Met Asn Val Val Ala Phe Val Thr
242                          1               5                  10
244 ctg atc atc tct ttt ctt ctg ctt tct cag gtaaactgtt aaaaccattt         583
245 Leu Ile Ile Ser Phe Leu Leu Leu Ser Gln
246              15                  20
248 tcaagactac cttttctcta tttcagacaa accaaagtaa aacaatgaaa aatctctctg     643
250 gtctttcata g gta ctt gca gag ttg tca tca tcc agc aac aat gaa act     693
251              Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn Glu Thr
252                          25                  30
254 tcc tct gtt tct cag gtaagagtga tacaaaaaca tactaaacaa actttcaaga     748
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255 Ser Ser Val Ser Gln
256 35
258 gagtaatata taaggaaatg ttggcttctt tttttgttg ctaatcag acg aat gac        805
259                                                        Thr Asn Asp
260                                                        40
262 gag aac caa act gcg gcg ttt aag aga aca tac cac cat cgt cca aga        853
263 Glu Asn Gln Thr Ala Ala Phe Lys Arg Thr Tyr His His Arg Pro Arg
264         45                  50                  55
266 atc agttagtcta ctctttcaac actctaattc ctttgttcta agtattttt           906
267 Ile
270 ttgccccca caacctttt tttattaaat gagccaattt ttatagat tgt ggg cat      963
271                                                      Cys Gly His
272                                                      60
274 gca tgc gca agg aga tgc agt aag aca tcg agg aag aaa gtt tgt cac      1011
275 Ala Cys Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His
276         65                  70                  75
278 aga gcc tgt gga agt tgt tgt gcc aag tgt cag tgt gtg ccg ccg gga      1059
279 Arg Ala Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly
280     80                  85                  90
282 acc tcc ggc aac aca gca tca tgt cct tgc tac gcc agt atc cgt aca      1107
283 Thr Ser Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr
284 95                  100                 105                 110
286 cat ggc aat aaa ctc aaa tgt cct taaaagactt ctcattctc aactatagtc     1161
287 His Gly Asn Lys Leu Lys Cys Pro
288                 115
290 tcatcttctg attatgtttc ttcttttgtt atgttgcatg tgtgatgtgt gagcttatta    1221
292 ttatgttgat tgttgacata attcaactat ataatttgta tcgattccga ataataagat    1281
294 gagtgatttt attggctatt aagttttttt ttttttttt tgggcacaat ggctattaag    1341
296 ttttaaacat ctgattttat tggttacaaa aaacaacaaa gtttcatttt catattaaca    1401
298 caaaatctcc atacatatta ccaaaccaaa aaaatacaca aggggagag agaccaacgg      1461
300 ttcttggttc agagtttgca tcttgtttga gccgtcaccg tttcttagac ttaacagcca    1521
302 caacaccttt ataaagcttc acgcgatcct tcaacgcatc tcgccgaggc cgagccacct    1581
304 tattgtttgg atcaaacaac aaaacttctt caaacgcatt caatgccaaa ggc           1634
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308 <211> LENGTH: 118
309 <212> TYPE: PRT
310 <213> ORGANISM: Arabidopsis thaliana
312 <400> SEQUENCE: 4
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318 Leu Leu Leu Ser Gln Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn
319             20                  25                  30
322 Glu Thr Ser Ser Val Ser Gln Thr Asn Asp Glu Asn Gln Thr Ala Ala
323             35                  40                  45
326 Phe Lys Arg Thr Tyr His His Arg Pro Arg Ile Cys Gly His Ala Cys
327         50                  55                  60
330 Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His Arg Ala
331 65                  70                  75                  80
334 Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly Thr Ser
```

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335                    85                   90                   95
338 Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr His Gly
339               100                 105                  110
342 Asn Lys Leu Lys Cys Pro
343         115
346 <210> SEQ ID NO: 5
347 <211> LENGTH: 1453
348 <212> TYPE: DNA
349 <213> ORGANISM: Arabidopsis thaliana
352 <220> FEATURE:
353 <221> NAME/KEY: CDS
354 <222> LOCATION: (501)..(533)
355 <223> OTHER INFORMATION: signal peptide (exon 1)
357 <220> FEATURE:
358 <221> NAME/KEY: CDS
359 <222> LOCATION: (664)..(691)
360 <223> OTHER INFORMATION: propeptide (exon 2)
362 <220> FEATURE:
363 <221> NAME/KEY: CDS
364 <222> LOCATION: (772)...(950)
365 <223> OTHER INFORMATION: conserved cysteine motif (exon 3)
367 <400> SEQUENCE: 5
368 gaaaaaaaga agaaaagata atggtccgta ttaatatagt tgaaaacttg aaactacttt          60
370 ttagtttgta tataatacag tagactaggg atccagttga gtttctttct ttattttgag         120
372 tttgtgttta tgtttgattt tacgtttta tatgtaaata agatatttta cgaattatgg         180
374 ttttatttgg gtagaagttg tagaatgact taaacaatca agtggcagaa tgagatatat         240
376 aaagtaatat aatatatgta ccgttattaa cttattgtac atgtgaatga ggaagcttac         300
378 acacacacac cttctataaa tagctgacaa aactggttgt tacacacaac acattcataa         360
380 atctctcaaa gtaagaacta agagctttac tacagtccta ctctctacac atcttctctc         420
382 tctctcaaga gctagtcatg gccaaactca taacttcttt tctcttactc acaattttat         480
384 tcactttcgt ttgtctcact atg tca aaa gaa gct gag tac cat cca gaa agt         533
385                           Met Ser Lys Glu Ala Glu Tyr His Pro Glu Ser
386                           1               5                  10
388 gtaagttttt attttttggt aaaatagaaa gtgtaagttt tataattcat tcaattgttt         593
390 ttgcctttcc ctttctattt attgctataa atctaatacc cgcgttaaaa tttgtttttga        653
392 aattaaacag tat gga cca gga agt ctg aaa tca tac c gtaagtaaaa              701
393             Tyr Gly Pro Gly Ser Leu Lys Ser Tyr
394                           15                  20
396 acttcttctt cttttatgaa tcttgtttct tattatatat caaataaaaa ctcgattatc        761
398 atgattgcag aa tgt gga gga caa tgc aca agg aga tgt agc aac aca           809
399                Gln Cys Gly Gly Gln Cys Thr Arg Arg Cys Ser Asn Thr
400                           25                  30
402 aag tat cat aag cca tgc atg ttc ttc tgc caa aag tgt tgt gct aaa         857
403 Lys Tyr His Lys Pro Cys Met Phe Phe Cys Gln Lys Cys Cys Ala Lys
404     35                  40                  45
406 tgc ctt tgt gtc cct cca ggc acg tac ggc aac aaa caa gtg tgt cct        905
407 Cys Leu Cys Val Pro Pro Gly Thr Tyr Gly Asn Lys Gln Val Cys Pro
408 50                  55                  60                  65
410 tgt tac aac aac tgg aag act caa caa ggt gga cca aaa tgt cca            950
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/19/2006
PATENT APPLICATION: **US/10/521,518**   TIME: 08:56:39

Input Set : **A:\294-208 PCT-US sequence listing.txt**
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:31; Xaa Pos. 37,38,39,41,44,45,46,47,48,49,50,52,53

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Val Gly Glu Gly Val Val Lys Ile
                35

tgtaaagtgt tatatctctg tttatatatg atttttaaac ggttaaaaac tagtcatatg  799

tgtataaata tatcatgtga ag at  tgc ggt ggg aga tgc aaa ggt aga tgc   850
                            Asp Cys Gly Gly Arg Cys Lys Gly Arg Cys
insert → 40                                  45

agc aaa tcg tcg agg cca aat ctg tgt ttg aga gca tgc aac agc tgt    898
Ser Lys Ser Ser Arg Pro Asn Leu Cys Leu Arg Ala Cys Asn Ser Cys
50              55                  60                  65

tgt tac cgc tgc aac tgt gtg cca cca ggc acc gcc ggg aac cac cac    946
Cys Tyr Arg Cys Asn Cys Val Pro Pro Gly Thr Ala Gly Asn His His
            70              75                  80

ctt tgt cct tgc tac gcc tcc att acc act cgt ggt ggc cgt ctc aag    994
Leu Cys Pro Cys Tyr Ala Ser Ile Thr Thr Arg Gly Gly Arg Leu Lys
        85              90              95

tgc cct taaacatata cacatacaga tgtgtgtata tgtcttccgc gagcacacac     1050
Cys Pro
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ggt gaa ggc gta gtg aaa atc g gtatgtaacc ctaacttata tataacacgt      745
Gly Glu Gly Val Val Lys Ile
        35

tggtatataa cttaatattt ctgatgggtg cactctcttc ccaacttata tatatctttg      805

ttatggagaa tgtctcaagc ttttaatgag atgttatatc tcggagaagg aaactatgaa      865

ctaaaagctt tggattcctt tgcaacaaat ataaactttt gatgggttta aacggattaa      925

attagttaca tgtgtttgat gaatgtatgt atgattgtag at  tgt ggt ggg aga      979
                                              Asp Cys Gly Gly Arg
                          insert 40

tgc aaa gat aga tgc agc aaa tct tcg aga acg aag cta tgc ttg aga     1027
Cys Lys Asp Arg Cys Ser Lys Ser Ser Arg Thr Lys Leu Cys Leu Arg
45                  50                  55                  60

gcg tgc aac agc tgt tgt tcc cgc tgc aac tgt gtg cca cct ggt act     1075
Ala Cys Asn Ser Cys Cys Ser Arg Cys Asn Cys Val Pro Pro Gly Thr
                65                  70                  75

tct gga aac acc cac ctt tgt cct tgc tac gcc tcc att acc act cac     1123
Ser Gly Asn Thr His Leu Cys Pro Cys Tyr Ala Ser Ile Thr Thr His
                80                  85                  90

ggt ggc cgc ctc aag tgc cct taaaatttct tctgtgtctg tttctgtttc     1174
Gly Gly Arg Leu Lys Cys Pro
                95
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gcg ccg cct gtc aaa cct cca aca cca cct ccc gta aga act cgg ata g    1391
Ala Pro Pro Val Lys Pro Pro Thr Pro Pro Pro Val Arg Thr Arg Ile
    200             205             210

gtaataataa ttttctttca aaagtgtgat gattatcggt cgttgattag atcggatgta    1451

taattggact aaattttgga cggtttag at  tgc gtg cct tta tgt ggg acg      1502
                                Asp Cys Val Pro Leu Cys Gly Thr
          insert → 215                              220

agg tgt ggg caa cac tcg agg aag aac gta tgt atg aga gcg tgc gtc    1550
Arg Cys Gly Gln His Ser Arg Lys Asn Val Cys Met Arg Ala Cys Val
        225             230             235

acg tgc tgc tac cgc tgc aag tgt gtt ccc cca ggc acc tac ggt aat    1598
Thr Cys Cys Tyr Arg Cys Lys Cys Val Pro Pro Gly Thr Tyr Gly Asn
    240             245             250

aag gag aag tgt gga tct tgt tac gcc aac atg aag aca cgt ggt gga    1646
Lys Glu Lys Cys Gly Ser Cys Tyr Ala Asn Met Lys Thr Arg Gly Gly
255             260             265             270

aaa tcc aaa tgt cct tgaaccttta tatgacgatg gttgttaaac gaaataattt    1701
Lys Ser Lys Cys Pro
            275
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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:517 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
L:1047 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 15
L:1311 .M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19
L:1312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1448 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1786 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:2187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:2191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:16
L:2195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:32
L:2199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:48